

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hammond, H. Kirk

Insel, Paul A.

Ping, Peipei

Post, Steven R.

Gao, Meihua

(ii) TITLE OF THE INVENTION: GENE THERAPY FOR CONGESTIVE HEART FAILURE

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: MORRISON & FOERSTER

(B) STREET: 755 PAGE MILL ROAD

(C) CITY: PALO ALTO

(D) STATE: CA

(E) COUNTRY: USA

(F) ZIP: 94304-1018

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette

(B) COMPUTER: IBM Compatible

(C) OPERATING SYSTEM: DOS

(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: UNKNOWN

(B) FILING DATE: HERewith

(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 09/472,667

(B) FILING DATE: December 27, 1999

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: POLIZZI, CATHERINE M.

(B) REGISTRATION NUMBER: 40,130

(C) REFERENCE/DOCKET NUMBER: 220002056723

(ix) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 314 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...312

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA
48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC
96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG
144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC
192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA NGC AAG GGC AAG
240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys
65 70 75 80

GAA CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAA GAT ACC GAA GTG
288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95

ACA ACG ACA CCG GCG GGA CCG CTG AA
Thr Thr Thr Pro Ala Gly Pro Leu
100

314

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
1 5 10 15
Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
20 25 30
Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
35 40 45
Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60
Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Xaa Lys Gly Lys
65 70 75 80
Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95
Thr Thr Thr Pro Ala Gly Pro Leu
100

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1812 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...1812

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC GGG GGC GCT
48

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala
1 5 10 15

TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG TGC CCT GTG
96

Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val
20 25 30

TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC ATG CGG GCT 144
Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala
35 40 45

GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG ATC TTG GCC 192
Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala
50 55 60

TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG CTC GGT GCC
240
Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
65 70 75 80

AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC TGC ACA CAC
288
Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
85 90 95

TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG ACC CGC AGT
336
Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
100 105 110

TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG CAG CAG GAG
384
Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu

115 120 125

CGG CTG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG GAG ATG AAA
432

Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys
130 135 140

GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG ATC TAC ATA
480

Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile
145 150 155 160

CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT GAG GGC TTC
528

Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe
165 170 175

ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC ATG ACC CTG
576

Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu
180 185 190

AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG AAT CAC TGC
624

Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys
195 200 205

CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG TCA GGG CTG
672

Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu
210 215 220

CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG ATG GGG GTA
720

Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val
225 230 235 240

GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA GGT GTG AAT
768

Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn
245 250 255

GTG AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC TGC GGC GTC
816

Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val

260 265 270

CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT GAT GTG ACC
864

Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr
275 280 285

CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC ATC CAC ATC
912

Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile
290 295 300

ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA GTG GAG CCA
960

Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro
305 310 315 320

GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG CAC ATT GAG
1008

Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu
325 330 335

ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG GAG AAA GGC
1056

Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly
340 345 350

ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG GAA GGG CTG
1104

Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu
355 360 365

ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC AAG GAC TCC
1152

Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser
370 375 380

AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA GAC AAC CGG
1200

Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg
385 390 395 400

GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT GAG TTC CTG
1248

Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu

405 410 415

AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG AAG GAC CAT
1296

Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His
420 425 430

GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT GAG AAG AAG
1344

Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys
435 440 445

TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT GCC TGT GCC
1392

Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala
450 455 460

CTG TTG GTC TTC TGC TTC ATC TGC TTC ATC CAG CTT CTA ATT TTC CCA 1440
Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro
465 470 475 480

CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC CTG CTG CTG
1488

His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu
485 490 495

CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT TCT CTG TTC 1536
Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
500 505 510

CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC TCA CGG GCA
1584

Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
515 520 525

CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG TTT ACT TCT 1632
His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
530 535 540

GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA CGG AGC TGT
1680

Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
545 550 555 560

GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT GCC TGC CAC
1728

Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
565 570 575

CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC CTG TGT GAG
1776

Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu
580 585 590

GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TTC
Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe
595 600

1812

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Val Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val Gly Gly Ala
1 5 10 15
Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp Cys Pro Val
20 25 30
Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg Met Arg Ala
35 40 45
Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu Ile Leu Ala
50 55 60
Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln Leu Gly Ala
65 70 75 80
Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile Cys Thr His
85 90 95
Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu Thr Arg Ser
100 105 110
Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg Gln Gln Glu
115 120 125
Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met Glu Met Lys

130 135 140
 Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys Ile Tyr Ile
 145 150 155 160
 Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe
 165 170 175
 Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val Met Thr Leu
 180 185 190
 Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu Asn His Cys
 195 200 205
 Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu
 210 215 220
 Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu Met Gly Val
 225 230 235 240
 Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr Gly Val Asn
 245 250 255
 Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His Cys Gly Val
 260 265 270
 Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn Asp Val Thr
 275 280 285
 Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg Ile His Ile
 290 295 300
 Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu Val Glu Pro
 305 310 315 320
 Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln His Ile Glu
 325 330 335
 Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu Glu Lys Gly
 340 345 350
 Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met Glu Gly Leu
 355 360 365
 Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr Lys Asp Ser
 370 375 380
 Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys Asp Asn Arg
 385 390 395 400
 Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp Glu Phe Leu
 405 410 415
 Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg Lys Asp His
 420 425 430
 Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe Glu Lys Lys
 435 440 445
 Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val Ala Cys Ala
 450 455 460
 Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu Ile Phe Pro
 465 470 475 480
 His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe Leu Leu Leu
 485 490 495

Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly Ser Leu Phe
 500 505 510
 Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg Ser Arg Ala
 515 520 525
 His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val Phe Thr Ser
 530 535 540
 Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile Arg Ser Cys
 545 550 555 560
 Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr Ala Cys His
 565 570 575
 Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro Leu Cys Glu
 580 585 590
 Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Phe
 595 600

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3549 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...3501
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG TCA TGG TTT AGT GGC CTC CTG GTC CCT AAA GTG GAT GAA CGG AAA
 48

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15

ACA GCC TGG GGT GAA CGC AAT GGG CAG AAG CGT TCG CGG CGC CGT GGC
 96

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30

ACT CGG GCA GGT GGC TTC TGC ACG CCC CGC TAT ATG AGC TGC CTC CGG
 144

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45

GAT GCA GAG CCA CCC AGC CCC ACC CCT GCG GGC CCC CCT CGG TGC CCC
192

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
50 55 60

TGG CAG GAT GAC GCC TTC ATC CGG AGG GGC GGC CCA GGC AAG GGC AAG
240

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
65 70 75 80

GAG CTG GGG CTG CGG GCA GTG GCC CTG GGC TTC GAG GAT ACC GAG GTG
288

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
85 90 95

ACA ACG ACA GCG GGC GGG ACG GCT GAG GTG GCG CCC GAC GCG GTG CCC
336

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
100 105 110

AGG AGT GGG CGA TCC TGC TGG CGC CGT TTG GTG CAG GTG TTC CAG TCG
384

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
115 120 125

AAG CAG TTC CGT TCG GCC AAG CTG GAG CGC CTG TAC CAG CGG TAC TTT
432

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
130 135 140

TTC CAG ATG AAC CAG AGC AGC CTG ACG CTG CTG GTG GCG GTG CTG GTG
480

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val
145 150 155 160

CTG CTC ACA GCG GTG CTG CTG GCT TTC CAA GCC GCA CCC GCC CGC CCT
528

Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro
165 170 175

CAG CCT GCC TAT GTG GCA CTG TTG GCC TGT GCC GCC GCC CTG TTC GTG
576

Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val
180 185 190

GGG CTC ATG GTG GTG TGT AAC CGG CAT AGC TTC CGC CAG GAC TCC ATG
624

Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
195 200 205

TGG GTG GTG AGT AAC GTG GTG CTG GGC ATC CTG GCG GCA GTG CAG GTC
672

Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
210 215 220

GGG GGC GCT TTC GCA GCA GAC CCG CGC AGC CCC TCT GCG GGC CTC TGG
720

Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
225 230 235 240

TGC CCT GTG TTC TTT GTA TAC ATC GCA TAC ACG CTC CTC CCC ATC CGC 768
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
245 250 255

ATG CGG GCT GCC GTC CTC AGC GGC CTG GGC CTC TCC ACC TTG CAT TTG
816

Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
260 265 270

ATC TTG GCC TGG CAA CTT AAC CGT GGT GAT GCC TTC CTC TGG AAG CAG
864

Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
275 280 285

CTC GGT GCC AAT GTG CTG CTG TTC CTC TGC ACC AAC GTC ATT AGC ATC 912
Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile
290 295 300

TGC ACA CAC TAT CCA GCA GAG GTG TCT CAG CGC CAG GCC TTT CAG GAG
960

Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
305 310 315 320

ACC CGC AGT TAC ATC CAG GCC CGG CTC CAC CTG CAG CAT GAG AAT CGG
1008

Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
325 330 335

CAG CAG GAG CGG CTG CTG CTG TCG GTA TTG CCC CAG CAC GTT GCC ATG
1056

Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met
340 345 350

GAG ATG AAA GAA GAC ATC AAC ACA AAA AAA GAA GAC ATG TTC CAC AAG
1104

Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys
355 360 365

ATC TAC ATA CAG AAG CAT GAC AAT GTC AGC ATC CTG TTT GCA GAC ATT
1152

Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile
370 375 380

GAG GGC TTC ACC AGC CTG GCA TCC CAG TGC ACT GCG CAG GAG CTG GTC
1200

Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val
385 390 395 400

ATG ACC CTG AAT GAG CTC TTT GCC CGG TTT GAC AAG CTG GCT GCG GAG
1248

Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu
405 410 415

AAT CAC TGC CTG AGG ATC AAG ATC TTG GGG GAC TGT TAC TAC TGT GTG
1296

Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val
420 425 430

TCA GGG CTG CCG GAG GCC CGG GCC GAC CAT GCC CAC TGC TGT GTG GAG
1344

Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu
435 440 445

ATG GGG GTA GAC ATG ATT GAG GCC ATC TCG CTG GTA CGT GAG GTG ACA
1392

Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr
450 455 460

GGT GTG AAT GTG AAC ATG CGC GTG GGC ATC CAC AGC GGG CGC GTG CAC
1440

Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His
465 470 475 480

TGC GGC GTC CTT GGC TTG CGG AAA TGG CAG TTC GAT GTG TGG TCC AAT
1488

Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn
485 490 495

GAT GTG ACC CTG GCC AAC CAC ATG GAA GCA GGA AGC CGG GCT GGC CGC
1536

Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg
500 505 510

ATC CAC ATC ACT CGG GCA ACA CTG CAG TAC CTG AAC GGG GAC TAC GAA
1584

Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu
515 520 525

GTG GAG CCA GGC CGT GGT GGC AAG CGC AAC GCG TAC CTC AAG GAG CAG
1632

Val Glu Pro Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln
530 535 540

CAC ATT GAG ACT TTC CTC ATC CTG GGC GCC AGC CAG AAA CGG AAA GAG
1680

His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu
545 550 555 560

GAG AAA GGC ATG CTG GCC AAG CTG CAG CGG ACT CGG GCC AAC TCC ATG
1728

Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met
565 570 575

GAA GGG CTG ATG CCG CGA TGG GTT CCT GAT CGT GCC TTC TCC CGG ACC
1776

Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr
580 585 590

AAG GAC TCC AAG GCC TTC CGC CAG ATG GGC ATT GAT GAT TCC AGC AAA
1824

Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys
595 600 605

GAC AAC CGG GGC ACC CAA GAT GCC CTG AAC CCT GAG GAT GAG GTG GAT
1872

Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp
610 615 620

GAG TTC CTG AGC CGT GCC ATC GAT GCC CGC AGC ATT GAT CAG CTG CGG
1920

Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg
625 630 635 640

AAG GAC CAT GTG CGC CGG TTT TTG CTC ACC TTC CAG AGA GAG GAT TTT
1968

Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe
645 650 655

GAG AAG AAG TAC TCC CGG AAG GTG GAT CCC CGC TTC GGA GCC TAC GTT
2016

Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val
660 665 670

GCC TGT GCC CTG TTG GTC TTC TGC TTC ATC TGC TTC ATC CAG CTT CTA 2064
Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu
675 680 685

ATT TTC CCA CAC TCC ACC CTG ATG CTT GGG ATT TAT GCC AGC ATC TTC 2112
Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe
690 695 700

CTG CTG CTG CTA ATC ACC GTG CTG ATC TGT GCT GTG TAC TCC TGT GGT
2160

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly
705 710 715 720

TCT CTG TTC CCT AAG GCC CTG CAA CGT CTG TCC CGC AGC ATT GTC CGC
2208

Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg
725 730 735

TCA CGG GCA CAT AGC ACC GCA GTT GGC ATC TTT TCC GTC CTG CTT GTG
2256

Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val
740 745 750

TTT ACT TCT GCC ATT GCC AAC ATG TTC ACC TGT AAC CAC ACC CCC ATA
2304

Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile
755 760 765

CGG AGC TGT GCA GCC CGG ATG CTG AAT TTA ACA CCT GCT GAC ATC ACT
2352

Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr
770 775 780

GCC TGC CAC CTG CAG CAG CTC AAT TAC TCT CTG GGC CTG GAT GCT CCC
2400

Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro
785 790 795 800

CTG TGT GAG GGC ACC ATG CCC ACC TGC AGC TTT CCT GAG GTG TCC ATC
2448

Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile
805 810 815

GGG AAC ATG CTG CTG AGT CTC TTG GCC AGC TCT GTC TTC CTG CAC ATC
2496

Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile
820 825 830

AGC AGC ATC GGG AAG TTG GCC ATG ATC TTT GTC TTG GGG CTC ATC TAT
2544

Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr
835 840 845

TTG GTG CTG CTT CTG CTG GGT CCC CCA GCC GCC ATC TTT GAC AAC TAT
2592

Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr
850 855 860

GAC CTA CTG CTT GGC GTC CAT GGC TTG GCT TCT TCC AAT GAG ACC TTT
2640

Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
865 870 875 880

GAT GGG CTG GAC TGT CCA GCT GCA GGG AGG GTG GCC CTC AAA TAT ATG
2688

Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
885 890 895

ACC CCT GTG ATT CTG CTG GTG TTT GCG CTG GCG CTG TAT CTG CAT GCT
2736

Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
900 905 910

CAG CAG GTG GAA TCG ACT GCC CGC CTA AAC TTC CTC TGG AAA CTA CAG
2784

Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln
 915 920 925

GCA ACA GGG GAA AAA GAG GAG ATG GAG GAG CTA CAG GCA TAC AAC CGG
 2832

Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940

AGG CTG CTG CAT AAC ATT CTG CCC AAG GAC GTG GCG GCC CAC TTC CTG
 2880

Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960

GCC CGG GAG CGC CGC AAT GAT GAA CTC TAC TAT CAG TCG TGT GAG TGT
 2928

Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975

GTG GCT GTT ATG TTT GCC TCC ATT GCC AAC TTC TCT GAG TTC TAT GTG 2976
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990

GAG CTG GAG GCA AAC AAT GAG GGT GCC GAG TGC CTG CGG CTG CTC AAC
 3024

Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Leu Asn
 995 1000 1005

GAG ATC ATC GCT GAC TTT GAT GAG ATT ATC AGC GAG GAG CGG TTC CGG
 3072

Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020

CAG CTG GAA AAG ATC AAG ACG ATT GGT AGC ACC TAC ATG GCT GCC TCA
 3120

Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 1025 1030 1035 1040

GGG CTG AAC GCC AGC ACC TAC GAT CAG GTG GGC CGC TCC CAC ATC ACT
 3168

Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055

GCC CTG GCT GAC TAC GCC ATG CGG CTC ATG GAG CAG ATG AAG CAC ATC
 3216

Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

1060 1065 1070

AAT GAG CAC TCC TTC AAC AAT TTC CAG ATG AAG ATT GGG CTG AAC ATG
3264

Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met
1075 1080 1085

GGC CCA GTC GTG GCA GGT GTC ATC GGG GCT CGG AAG CCA CAG TAT GAC
3312

Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp
1090 1095 1100

ATC TGG GGG AAC ACA GTG AAT GTC TCT AGT CGT ATG GAC AGC ACG GGG
3360

Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly
1105 1110 1115 1120

GTC CCC GAC CGA ATC CAG GTG ACC ACG GAC CTG TAC CAG GTT CTA GCT
3408

Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala
1125 1130 1135

GCC AAG GGC TAC CAG CTG GAG TGT CGA GGG GTG GTC AAG GTG AAG GGC
3456

Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly
1140 1145 1150

AAG GGG GAG ATG ACC ACC TAC TTC CTC AAT GGG GGC CCC AGC AGT TAACA
3506

Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
1155 1160 1165

GGGCCCAGCC ACAAATTCAG CTGAAGGGAC CAAGGTGGGC ACT 3549

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1167 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
 50 55 60
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
 65 70 75 80
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
 85 90 95
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
 100 105 110
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
 115 120 125
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
 130 135 140
 Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Val Ala Val Leu Val
 145 150 155 160
 Leu Leu Thr Ala Val Leu Leu Ala Phe Gln Ala Ala Pro Ala Arg Pro
 165 170 175
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val
 180 185 190
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
 195 200 205
 Trp Val Val Ser Asn Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
 210 215 220
 Gly Gly Ala Phe Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
 225 230 235 240
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
 245 250 255
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
 260 265 270
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Ser Ile
 290 295 300
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320
 Thr Arg Ser Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met

340 345 350
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Phe His Lys
 355 360 365
 Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp Ile
 370 375 380
 Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu Val
 385 390 395 400
 Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala Glu
 405 410 415
 Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys Val
 420 425 430
 Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val Glu
 435 440 445
 Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val Thr
 450 455 460
 Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val His
 465 470 475 480
 Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser Asn
 485 490 495
 Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Ser Arg Ala Gly Arg
 500 505 510
 Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu
 515 520 525
 Val Glu Pro Gly Arg Gly Gly Lys Arg Asn Ala Tyr Leu Lys Glu Gln
 530 535 540
 His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu
 545 550 555 560
 Glu Lys Gly Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met
 565 570 575
 Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr
 580 585 590
 Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys
 595 600 605
 Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp
 610 615 620
 Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg
 625 630 635 640
 Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Phe
 645 650 655
 Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val
 660 665 670
 Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu
 675 680 685
 Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe
 690 695 700

Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly
 705 710 715 720
 Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg
 725 730 735
 Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val
 740 745 750
 Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile
 755 760 765
 Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr
 770 775 780
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro
 785 790 795 800
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Val Ser Ile
 805 810 815
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile
 820 825 830
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr
 835 840 845
 Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Ala Ile Phe Asp Asn Tyr
 850 855 860
 Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
 865 870 875 880
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
 885 890 895
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
 900 905 910
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asn Phe Leu Trp Lys Leu Gln
 915 920 925
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990
 Glu Leu Glu Ala Asn Asn Glu Gly Ala Glu Cys Leu Arg Leu Leu Asn
 995 1000 1005
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 025 1030 1035 1040
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile

1060 1065 1070
 Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met
 1075 1080 1085
 Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp
 1090 1095 1100
 Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly
 105 1110 1115 1120
 Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala
 1125 1130 1135
 Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly
 1140 1145 1150
 Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
 1155 1160 1165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACGTAGAATT CGGRGAYTGT TAYTACTG

28

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACGTTAAGCT TCCASACRTC RAAYTGCCA

29

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic RNA
 (ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

UUAUUUAAWW

9

<210> 10
 <211> 3552
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(3507)

<400> SEQ ID NO:10

atg tca tgg ttg agt ggc ctc ctg gtc cct aaa gtg gat gaa cgg aaa 48
 Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15

aca gcc tgg ggt gaa cgc aat ggg cag aag cgt tgc cgg cgc cgt ggc 96
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30

act cgg gca ggt ggc ttc tgc acg ccc cgc tat atg agc tgc ctc cgg 144
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45

gat gca gag cca ccc agc ccc acc cct gcg ggc ccc cct cgg tgc ccc 192
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
 50 55 60

tgg cag gat gac gcc ttc atc cgg agg ggc ggc cca ggc aag ggc aag 240
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
 65 70 75 80

gag ctg ggg ctg cgg gca gtg gcc ctg ggc ttc gag gat acc gag gtg 288
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

aca acg aca gcg ggc ggg acg gct gag gtg gcg ccc gac gcg gtg ccc 336
Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
100 105 110

agg agt ggg cga tcc tgc tgg cgc cgt ctg gtg cag gtg ttc cag tcg 384
Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
115 120 125

aag cag ttc cgt tcg gcc aag ctg gag cgc ctg tac cag cgg tac ttc 432
Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
130 135 140

ttc cag atg aac cag agc agc ctg acg ctg ctg atg gcg gtg ctg gtg 480
Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val
145 150 155 160

ctg ctc aca gcg gtg ctg ctg gct ttc cac gcc gca ccc gcc cgc cct 528
Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro
165 170 175

cag cct gcc tat gtg gca ctg ttg gcc tgt gcc gcc gcc ctg ttc gtg 576
Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val
180 185 190

ggg ctc atg gtg gtg tgt aac cgg cat agc ttc cgc cag gac tcc atg 624
Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
195 200 205

tgg gtg gtg agt tac gtg gtg ctg ggc atc ctg gcg gca gtg cag gtc 672
Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
210 215 220

ggg ggc gct ctc gca gca gac ccg cgc agc ccc tct gcg ggc ctc tgg 720
Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
225 230 235 240

tgc cct gtg ttc ttt gtc tac atc gcc tac acg ctc ctc ccc atc cgc 768
Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
245 250 255

atg cgg gct gcc gtc ctc agc ggc ctg ggc ctc tcc acc ttg cat ttg 816
Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
260 265 270

atc ttg gcc tgg caa ctt aac cgt ggt gat gcc ttc ctc tgg aag cag 864
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285

ctc ggt gcc aat gtg ctg ctg ttc ctc tgc acc aac gtc att ggc atc 912
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile
 290 295 300

tgc aca cac tat cca gca gag gtg tct cag cgc cag gcc ttt cag gag 960
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320

acc cgc ggt tac atc cag gcc cgg ctc cac ctg cag cat gag aat cgg 1008
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335

cag cag gag cgg ctg ctg ctg tgc gta ttg ccc cag cac gtt gcc atg 1056
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met
 340 345 350

gag atg aaa gaa gac atc aac aca aaa aaa gaa gac atg atg ttc cac 1104
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His
 355 360 365

aag atc tac ata cag aag cat gac aat gtc agc atc ctg ttt gca gac 1152
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp
 370 375 380

att gag ggc ttc acc agc ctg gca tcc cag tgc act gcg cag gag ctg 1200
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu
 385 390 395 400

gtc atg acc ctg aat gag ctc ttt gcc cgg ttt gac aag ctg gct gcg 1248
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala
 405 410 415

gag aat cac tgc ctg agg atc aag atc ttg ggg gac tgt tac tac tgt 1296
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys
 420 425 430

gtg tca ggg ctg ccg gag gcc cgg gcc gac cat gcc cac tgc tgt gtg 1344
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val
 435 440 445

gag atg ggg gta gac atg att gag gcc atc tcg ctg gta cgt gag gtg 1392
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val
 450 455 460

aca ggt gtg aat gtg aac atg cgc gtg ggc atc cac agc ggg cgc gtg 1440
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val
 465 470 475 480

cac tgc ggc gtc ctt ggc ttg cgg aaa tgg cag ttc gat gtg tgg tcc 1488
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser
 485 490 495

aat gat gtg acc ctg gcc aac cac atg gag gca gga ggc cgg gct ggc 1536
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Arg Ala Gly
 500 505 510

cgc atc cac atc act cgg gca aca ctg cag tac ctg aac ggg gac tac 1584
 Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr
 515 520 525

gag gtg gag cca ggc cgt ggt ggc gag cgc aac gcg tac ctc aag gag 1632
 Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu
 530 535 540

cag cac att gag act ttc ctc atc ctg ggc gcc agc cag aaa cgg aaa 1680
 Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys
 545 550 555 560

gag gag aag gcc atg ctg gcc aag ctg cag cgg act cgg gcc aac tcc 1728
 Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser
 565 570 575

atg gaa ggg ctg atg ccg cgc tgg gtt cct gat cgt gcc ttc tcc cgg 1776
 Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg
 580 585 590

acc aag gac tcc aag gcc ttc cgc cag atg ggc att gat gat tcc agc 1824
 Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser
 595 600 605

aaa gac aac cgg ggc acc caa gat gcc ctg aac cct gag gat gag gtg 1872
 Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val
 610 615 620

gat gag ttc ctg agc cgt gcc atc gat gcc cgc agc att gat cag ctg 1920

Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu
625 630 635 640

cgg aag gac cat gtg cgc cgg ttt ctg ctc acc ttc cag aga gag gat 1968
Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp
645 650 655

ctt gag aag aag tac tcc cgg aag gtg gat ccc cgc ttc gga gcc tac 2016
Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr
660 665 670

gtt gcc tgt gcc ctg ttg gtc ttc tgc ttc atc tgc ttc atc cag ctt 2064
Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu
675 680 685

ctc atc ttc cca cac tcc acc ctg atg ctt ggg atc tat gcc agc atc 2112
Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile
690 695 700

ttc ctg ctg ctg cta atc acc gtg ctg atc tgt gct gtg tac tcc tgt 2160
Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys
705 710 715 720

ggt tct ctg ttc cct aag gcc ctg caa cgt ctg tcc cgc agc att gtc 2208
Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val
725 730 735

cgc tca cgg gca cat agc acc gca gtt ggc atc ttt tcc gtc ctg ctt 2256
Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu
740 745 750

gtg ttt act tct gcc att gcc aac atg ttc acc tgt aac cac acc ccc 2304
Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro
755 760 765

ata cgg agc tgt gca gcc cgg atg ctg aat tta aca cct gct gac atc 2352
Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile
770 775 780

act gcc tgc cac ctg cag cag ctc aat tac tct ctg ggc ctg gat gct 2400
Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala
785 790 795 800

ccc ctg tgt gag ggc acc atg ccc acc tgc agc ttt cct gag tac ttc 2448
Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe

805 810 815

atc ggg aac atg ctg ctg agt ctc ttg gcc agc tct gtc ttc ctg cac 2496
 Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His
 820 825 830

atc agc agc atc ggg aag ttg gcc atg atc ttt gtc ttg ggg ctc atc 2544
 Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile
 835 840 845

tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc acc atc ttt gac aac 2592
 Tyr Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn
 850 855 860

tat gac cta ctg ctt ggc gtc cat ggc ttg gct tct tcc aat gag acc 2640
 Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr
 865 870 875 880

ttt gat ggg ctg gac tgt cca gct gca ggg agg gtg gcc ctc aaa tat 2688
 Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr
 885 890 895

atg acc cct gtg att ctg ctg gtg ttt gcg ctg gcg ctg tat ctg cat 2736
 Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His
 900 905 910

gct cag cag gtg gag tcg act gcc cgc cta gac ttc ctc tgg aaa cta 2784
 Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu
 915 920 925

cag gca aca ggg gag aag gag gag atg gag gag cta cag gca tac aac 2832
 Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn
 930 935 940

cgg agg ctg ctg cat aac att ctg ccc aag gac gtg gcg gcc cac ttc 2880
 Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe
 945 950 955 960

ctg gcc cgg gag cgc cgc aat gat gaa ctc tac tat cag tcg tgt gag 2928
 Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu
 965 970 975

tgt gtg gct gtt atg ttt gcc tcc att gcc aac ttc tct gag ttc tat 2976
 Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr
 980 985 990

gtg gag ctg gag gca aac aat gag ggt gtc gag tgc ctg cgg ctg ctc 3024
Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu
995 1000 1005

aac gag atc atc gct gac ttt gat gag att atc agc gag gag cgg ttc 3072
Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe
1010 1015 1020

cgg cag ctg gaa aag atc aag acg att ggt agc acc tac atg gct gcc 3120
Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala
1025 1030 1035 1040

tca ggg ctg aac gcc agc acc tac gat cag gtg ggc cgc tcc cac atc 3168
Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile
1045 1050 1055

act gcc ctg gct gac tac gcc atg cgg ctc atg gag cag atg aag cac 3216
Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His
1060 1065 1070

atc aat gag cac tcc ttc aac aat ttc cag atg aag att ggg ctg aac 3264
Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn
1075 1080 1085

atg ggc cca gtc gtg gca ggt gtc atc ggg gct cgg aag cca cag tat 3312
Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr
1090 1095 1100

gac atc tgg ggg aac aca gtg aat gtc tct agt cgt atg gac agc acg 3360
Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr
1105 1110 1115 1120

ggg gtc ccc gac cga atc cag gtg acc acg gac ctg tac cag gtt cta 3408
Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu
1125 1130 1135

gct gcc aag ggc tac cag ctg gag tgt cga ggg gtg gtc aag gtg aag 3456
Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys
1140 1145 1150

ggc aag ggg gag atg acc acc tac ttc ctc aat ggg ggc ccc agc agt 3504
Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
1155 1160 1165

taa cagggcccag ccacaaattc agctgaaggg accaaggtgg gcact 3552

<210> 11

<211> 1168

<212> PRT

<213> Homo sapiens

<400> SEQ ID NO:11

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys

1 5 10 15

Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly

20 25 30

Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg

35 40 45

Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro

50 55 60

Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys

65 70 75 80

Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val

85 90 95

Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro

100 105 110

Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser

115 120 125

Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe

130 135 140

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val

145 150 155 160

Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro

165 170 175

Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val

180 185 190

Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met

195 200 205

Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val

210 215 220

Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp

225 230 235 240

Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg

245 250 255

Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu

260 265 270

Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln

275 280 285
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile
 290 295 300
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met
 340 345 350
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His
 355 360 365
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp
 370 375 380
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu
 385 390 395 400
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala
 405 410 415
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys
 420 425 430
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val
 435 440 445
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val
 450 455 460
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val
 465 470 475 480
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser
 485 490 495
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Arg Ala Gly
 500 505 510
 Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr
 515 520 525
 Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu
 530 535 540
 Gln His Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys
 545 550 555 560
 Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser
 565 570 575
 Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg
 580 585 590
 Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser
 595 600 605
 Lys Asp Asn Arg Gly Thr Gln Asp Ala Leu Asn Pro Glu Asp Glu Val
 610 615 620
 Asp Glu Phe Leu Ser Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu
 625 630 635 640

Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp
 645 650 655
 Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr
 660 665 670
 Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu
 675 680 685
 Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile
 690 695 700
 Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys
 705 710 715 720
 Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val
 725 730 735
 Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu
 740 745 750
 Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro
 755 760 765
 Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile
 770 775 780
 Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala
 785 790 795 800
 Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe
 805 810 815
 Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His
 820 825 830
 Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile
 835 840 845
 Tyr Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn
 850 855 860
 Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr
 865 870 875 880
 Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr
 885 890 895
 Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His
 900 905 910
 Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu
 915 920 925
 Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn
 930 935 940
 Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe
 945 950 955 960
 Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu
 965 970 975
 Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr
 980 985 990
 Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu

995 1000 1005
 Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe
 1010 1015 1020
 Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala
 1025 1030 1035 1040
 Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile
 1045 1050 1055
 Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His
 1060 1065 1070
 Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn
 1075 1080 1085
 Met Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr
 1090 1095 1100
 Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr
 1105 1110 1115 1120
 Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu
 1125 1130 1135
 Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys
 1140 1145 1150
 Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
 1155 1160 1165

<210> 12
 <211> 3582
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (22)..(3525)

<220>
 <223> Description of Artificial Sequence: Modified AC-VI

<400> SEQ ID NO:12
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 Met Ser Trp Phe Ser Gly Leu Leu Val Pro
 1 5 10

aaa gtg gat gaa cgg aaa aca gcc tgg ggt gaa cgc aat ggg cag aag 99
 Lys Val Asp Glu Arg Lys Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys
 15 20 25

cgt tcg cgg cgc cgt ggc act cgg gca ggt ggc ttc tgc acg ccc cgc 147

Arg Ser Arg Arg Arg Gly Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg
30 35 40

tat atg agc tgc ctc cgg gat gca gag cca ccc agc ccc acc cct gcg 195
Tyr Met Ser Cys Leu Arg Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala
45 50 55

ggc ccc cct cgg tgc ccc tgg cag gat gac gcc ttc atc cgg agg ggc 243
Gly Pro Pro Arg Cys Pro Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly
60 65 70

ggc cca ggc aag ggc aag gag ctg ggg ctg cgg gca gtg gcc ctg ggc 291
Gly Pro Gly Lys Gly Lys Glu Leu Gly Leu Arg Ala Val Ala Leu Gly
75 80 85 90

ttc gag gat acc gag gtg aca acg aca gcg ggc ggg acg gct gag gtg 339
Phe Glu Asp Thr Glu Val Thr Thr Thr Ala Gly Gly Thr Ala Glu Val
95 100 105

gcg ccc gac gcg gtg ccc agg agt ggg cga tcc tgc tgg cgc cgt ctg 387
Ala Pro Asp Ala Val Pro Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu
110 115 120

gtg cag gtg ttc cag tgc aag cag ttc cgt tgc gcc aag ctg gag cgc 435
Val Gln Val Phe Gln Ser Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg
125 130 135

ctg tac cag cgg tac ttc ttc cag atg aac cag agc agc ctg acg ctg 483
Leu Tyr Gln Arg Tyr Phe Phe Gln Met Asn Gln Ser Ser Leu Thr Leu
140 145 150

ctg atg gcg gtg ctg gtg ctg ctc aca gcg gtg ctg ctg gct ttc cac 531
Leu Met Ala Val Leu Val Leu Leu Thr Ala Val Leu Leu Ala Phe His
155 160 165 170

gcc gca ccc gcc cgc cct cag cct gcc tat gtg gca ctg ttg gcc tgt 579
Ala Ala Pro Ala Arg Pro Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys
175 180 185

gcc gcc gcc ctg ttc gtg ggg ctc atg gtg gtg tgt aac cgg cat agc 627
Ala Ala Ala Leu Phe Val Gly Leu Met Val Val Cys Asn Arg His Ser
190 195 200

ttc cgc cag gac tcc atg tgg gtg gtg agt tac gtg gtg ctg ggc atc 675
Phe Arg Gln Asp Ser Met Trp Val Val Ser Tyr Val Val Leu Gly Ile

205 210 215
 ctg gcg gca gtg cag gtc ggg ggc gct ctc gca gca gac ccg cgc agc 723
 Leu Ala Ala Val Gln Val Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser
 220 225 230

 ccc tct gcg ggc ctc tgg tgc cct gtg ttc ttt gtc tac atc gcc tac 771
 Pro Ser Ala Gly Leu Trp Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr
 235 240 245 250

 acg ctc ctc ccc atc cgc atg cgg gct gcc gtc ctc agc ggc ctg ggc 819
 Thr Leu Leu Pro Ile Arg Met Arg Ala Ala Val Leu Ser Gly Leu Gly
 255 260 265

 ctc tcc acc ttg cat ttg atc ttg gcc tgg caa ctt aac cgt ggt gat 867
 Leu Ser Thr Leu His Leu Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp
 270 275 280

 gcc ttc ctc tgg aag cag ctc ggt gcc aat gtg ctg ctg ttc ctc tgc 915
 Ala Phe Leu Trp Lys Gln Leu Gly Ala Asn Val Leu Leu Phe Leu Cys
 285 290 295

 acc aac gtc att ggc atc tgc aca cac tat cca gca gag gtg tct cag 963
 Thr Asn Val Ile Gly Ile Cys Thr His Tyr Pro Ala Glu Val Ser Gln
 300 305 310

 cgc cag gcc ttt cag gag acc cgc ggt tac atc cag gcc cgg ctc cac 1011
 Arg Gln Ala Phe Gln Glu Thr Arg Gly Tyr Ile Gln Ala Arg Leu His
 315 320 325 330

 ctg cag cat gag aat cgg cag cag gag cgg ctg ctg ctg tgc gta ttg 1059
 Leu Gln His Glu Asn Arg Gln Gln Glu Arg Leu Leu Leu Ser Val Leu
 335 340 345

 ccc cag cac gtt gcc atg gag atg aaa gaa gac atc aac aca aaa aaa 1107
 Pro Gln His Val Ala Met Glu Met Lys Glu Asp Ile Asn Thr Lys Lys
 350 355 360

 gaa gac atg atg ttc cac aag atc tac ata cag aag cat gac aat gtc 1155
 Glu Asp Met Met Phe His Lys Ile Tyr Ile Gln Lys His Asp Asn Val
 365 370 375

 agc atc ctg ttt gca gac att gag ggc ttc acc agc ctg gca tcc cag 1203
 Ser Ile Leu Phe Ala Asp Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln
 380 385 390

tgc act gcg cag gag ctg gtc atg acc ttg aat gag ctc ttt gcc cgg 1251
 Cys Thr Ala Gln Glu Leu Val Met Thr Leu Asn Glu Leu Phe Ala Arg
 395 400 405 410

ttt gac aag ctg gct gcg gag aat cac tgt ctg agg atc aag atc tta 1299
 Phe Asp Lys Leu Ala Ala Glu Asn His Cys Leu Arg Ile Lys Ile Leu
 415 420 425

gga gac tgt tac tac tgc gtg tca ggg ctg ccc gag gcc cgg gca gat 1347
 Gly Asp Cys Tyr Tyr Cys Val Ser Gly Leu Pro Glu Ala Arg Ala Asp
 430 435 440

cac gcc cac tgc tgt gtg gag atg ggg gta gac atg atc gaa gcc atc 1395
 His Ala His Cys Cys Val Glu Met Gly Val Asp Met Ile Glu Ala Ile
 445 450 455

tcg ctg gtg cgt gag gta aca ggt gtg aac gtg aac atg cgt gtg ggc 1443
 Ser Leu Val Arg Glu Val Thr Gly Val Asn Val Asn Met Arg Val Gly
 460 465 470

atc cac agc gga cgt gtg cat tgc ggc gtc ctt ggc cta cgg aaa tgg 1491
 Ile His Ser Gly Arg Val His Cys Gly Val Leu Gly Leu Arg Lys Trp
 475 480 485 490

cag ttt gat gtc tgg tca aac gat gtg acc ctg gct aac cac atg gag 1539
 Gln Phe Asp Val Trp Ser Asn Asp Val Thr Leu Ala Asn His Met Glu
 495 500 505

gcc ggg ggc ggc cgg cgc atc cac atc act cgg gct aca ctg cag tac 1587
 Ala Gly Gly Gly Arg Arg Ile His Ile Thr Arg Ala Thr Leu Gln Tyr
 510 515 520

ttg aac ggg gac tat gag gtg gag cca ggc cgt ggt ggt gaa cgc aat 1635
 Leu Asn Gly Asp Tyr Glu Val Glu Pro Gly Arg Gly Gly Glu Arg Asn
 525 530 535

gcg tac ctc aag gag cag tgc att gag acc ttc ctc ata ctt ggc gcc 1683
 Ala Tyr Leu Lys Glu Gln Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala
 540 545 550

agc caa aaa cgg aaa gag gag aaa gcc atg ctg gcc aag ctt cag cgg 1731
 Ser Gln Lys Arg Lys Glu Glu Lys Ala Met Leu Ala Lys Leu Gln Arg
 555 560 565 570

aca cgg gcc aac tcc atg gaa gga ctg atg ccc cgc tgg gtt cct gac 1779
 Thr Arg Ala Asn Ser Met Glu Gly Leu Met Pro Arg Trp Val Pro Asp
 575 580 585

cgt gcc ttc tcc cgg acc aag gac tct aag gca ttc cgc cag atg ggc 1827
 Arg Ala Phe Ser Arg Thr Lys Asp Ser Lys Ala Phe Arg Gln Met Gly
 590 595 600

att gat gat tct agc aaa gac aac cgg ggt gcc caa gat gct ctg aac 1875
 Ile Asp Asp Ser Ser Lys Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn
 605 610 615

cct gaa gat gag gtg gat gag ttc ctg ggc cga gcc atc gat gcc cgc 1923
 Pro Glu Asp Glu Val Asp Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg
 620 625 630

agc att gat cag ctg cgg aag gac cat gtg cgc cgg ttt ctg ctc acc 1971
 Ser Ile Asp Gln Leu Arg Lys Asp His Val Arg Arg Phe Leu Leu Thr
 635 640 645 650

ttc cag aga gag gat ctt gag aag aag tac tcc cgg aag gtg gat ccc 2019
 Phe Gln Arg Glu Asp Leu Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro
 655 660 665

cgc ttc gga gcc tac gtt gcc tgt gcc ctg ttg gtc ttc tgc ttc atc 2067
 Arg Phe Gly Ala Tyr Val Ala Cys Ala Leu Leu Val Phe Cys Phe Ile
 670 675 680

tgc ttc atc cag ctt ctc atc ttc cca cac tcc acc ctg atg ctt ggg 2115
 Cys Phe Ile Gln Leu Leu Ile Phe Pro His Ser Thr Leu Met Leu Gly
 685 690 695

atc tat gcc agc atc ttc ctg ctg ctg cta atc acc gtg ctg atc tgt 2163
 Ile Tyr Ala Ser Ile Phe Leu Leu Leu Leu Ile Thr Val Leu Ile Cys
 700 705 710

gct gtg tac tcc tgt ggt tct ctg ttc cct aag gcc ctg caa cgt ctg 2211
 Ala Val Tyr Ser Cys Gly Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu
 715 720 725 730

tcc cgc agc att gtc cgc tca cgg gca cat agc acc gca gtt ggc atc 2259
 Ser Arg Ser Ile Val Arg Ser Arg Ala His Ser Thr Ala Val Gly Ile
 735 740 745

ttt tcc gtc ctg ctt gtg ttt act tct gcc att gcc aac atg ttc acc 2307

Phe Ser Val Leu Leu Val Phe Thr Ser Ala Ile Ala Asn Met Phe Thr
750 755 760

tgt aac cac acc ccc ata cgg agc tgt gca gcc cgg atg ctg aat tta 2355
Cys Asn His Thr Pro Ile Arg Ser Cys Ala Ala Arg Met Leu Asn Leu
765 770 775

aca cct gct gac atc act gcc tgc cac ctg cag cag ctc aat tac tct 2403
Thr Pro Ala Asp Ile Thr Ala Cys His Leu Gln Gln Leu Asn Tyr Ser
780 785 790

ctg gcc ctg gat gct ccc ctg tgt gag gcc acc atg ccc acc tgc agc 2451
Leu Gly Leu Asp Ala Pro Leu Cys Glu Gly Thr Met Pro Thr Cys Ser
795 800 805 810

ttt cct gag tac ttc atc ggg aac atg ctg ctg agt ctc ttg gcc agc 2499
Phe Pro Glu Tyr Phe Ile Gly Asn Met Leu Leu Ser Leu Leu Ala Ser
815 820 825

tct gtc ttc ctg cac atc agc agc atc ggg aag ttg gcc atg atc ttt 2547
Ser Val Phe Leu His Ile Ser Ser Ile Gly Lys Leu Ala Met Ile Phe
830 835 840

gtc ttg ggg ctc atc tat ttg gtg ctg ctt ctg ctg ggt ccc cca gcc 2595
Val Leu Gly Leu Ile Tyr Leu Val Leu Leu Leu Gly Pro Pro Ala
845 850 855

acc atc ttt gac aac tat gac cta ctg ctt ggc gtc cat ggc ttg gct 2643
Thr Ile Phe Asp Asn Tyr Asp Leu Leu Leu Gly Val His Gly Leu Ala
860 865 870

tct tcc aat gag acc ttt gat ggg ctg gac tgt cca gct gca ggg agg 2691
Ser Ser Asn Glu Thr Phe Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg
875 880 885 890

gtg gcc ctc aaa tat atg acc cct gtg att ctg ctg gtg ttt gcg ctg 2739
Val Ala Leu Lys Tyr Met Thr Pro Val Ile Leu Leu Val Phe Ala Leu
895 900 905

ggc ctg tat ctg cat gct cag cag gtg gag tcg act gcc cgc cta gac 2787
Ala Leu Tyr Leu His Ala Gln Gln Val Glu Ser Thr Ala Arg Leu Asp
910 915 920

ttc ctc tgg aaa cta cag gca aca ggg gag aag gag gag atg gag gag 2835
Phe Leu Trp Lys Leu Gln Ala Thr Gly Glu Lys Glu Glu Met Glu Glu

925 930 935

cta cag gca tac aac cgg agg ctg ctg cat aac att ctg ccc aag gac 2883
Leu Gln Ala Tyr Asn Arg Arg Leu Leu His Asn Ile Leu Pro Lys Asp
940 945 950

gtg gcg gcc cac ttc ctg gcc cgg gag cgc cgc aat gat gaa ctc tac 2931
Val Ala Ala His Phe Leu Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr
955 960 965 970

tat cag tcg tgt gag tgt gtg gct gtt atg ttt gcc tcc att gcc aac 2979
Tyr Gln Ser Cys Glu Cys Val Ala Val Met Phe Ala Ser Ile Ala Asn
975 980 985

ttc tct gag ttc tat gtg gag ctg gag gca aac aat gag ggt gtc gag 3027
Phe Ser Glu Phe Tyr Val Glu Leu Glu Ala Asn Asn Glu Gly Val Glu
990 995 1000

tgc ctg cgg ctg ctc aac gag atc atc gct gac ttt gat gag att atc 3075
Cys Leu Arg Leu Leu Asn Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile
1005 1010 1015

agc gag gag cgg ttc cgg cag ctg gaa aag atc aag acg att ggt agc 3123
Ser Glu Glu Arg Phe Arg Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser
1020 1025 1030

acc tac atg gct gcc tca ggg ctg aac gcc agc acc tac gat cag gtg 3171
Thr Tyr Met Ala Ala Ser Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val
1035 1040 1045 1050

ggc cgc tcc cac atc act gcc ctg gct gac tac gcc atg cgg ctc atg 3219
Gly Arg Ser His Ile Thr Ala Leu Ala Asp Tyr Ala Met Arg Leu Met
1055 1060 1065

gag cag atg aag cac atc aat gag cac tcc ttc aac aat ttc cag atg 3267
Glu Gln Met Lys His Ile Asn Glu His Ser Phe Asn Asn Phe Gln Met
1070 1075 1080

aag att ggg ctg aac atg ggc cca gtc gtg gca ggt gtc atc ggg gct 3315
Lys Ile Gly Leu Asn Met Gly Pro Val Val Ala Gly Val Ile Gly Ala
1085 1090 1095

cgg aag cca cag tat gac atc tgg ggg aac aca gtg aat gtc tct agt 3363
Arg Lys Pro Gln Tyr Asp Ile Trp Gly Asn Thr Val Asn Val Ser Ser
1100 1105 1110

cgt atg gac agc acg ggg gtc ccc gac cga atc cag gtg acc acg gac 3411
 Arg Met Asp Ser Thr Gly Val Pro Asp Arg Ile Gln Val Thr Thr Asp
 1115 1120 1125 1130

ctg tac cag gtt cta gct gcc aag ggc tac cag ctg gag tgt cga ggg 3459
 Leu Tyr Gln Val Leu Ala Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly
 1135 1140 1145

gtg gtc aag gtg aag ggc aag ggg gag atg acc acc tac ttc ctc aat 3507
 Val Val Lys Val Lys Gly Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn
 1150 1155 1160

ggg ggc ccc agc agt taa cagggcccag ccacaaattc agctgaaggg 3555
 Gly Gly Pro Ser Ser
 1165

accaaggtgg gcactaaggg cgaattc 3582

<210> 13

<211> 1167

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: Modified AC-VI

<400> SEQ ID NO:13

Met Ser Trp Phe Ser Gly Leu Leu Val Pro Lys Val Asp Glu Arg Lys
 1 5 10 15
 Thr Ala Trp Gly Glu Arg Asn Gly Gln Lys Arg Ser Arg Arg Arg Gly
 20 25 30
 Thr Arg Ala Gly Gly Phe Cys Thr Pro Arg Tyr Met Ser Cys Leu Arg
 35 40 45
 Asp Ala Glu Pro Pro Ser Pro Thr Pro Ala Gly Pro Pro Arg Cys Pro
 50 55 60
 Trp Gln Asp Asp Ala Phe Ile Arg Arg Gly Gly Pro Gly Lys Gly Lys
 65 70 75 80
 Glu Leu Gly Leu Arg Ala Val Ala Leu Gly Phe Glu Asp Thr Glu Val
 85 90 95
 Thr Thr Thr Ala Gly Gly Thr Ala Glu Val Ala Pro Asp Ala Val Pro
 100 105 110
 Arg Ser Gly Arg Ser Cys Trp Arg Arg Leu Val Gln Val Phe Gln Ser
 115 120 125
 Lys Gln Phe Arg Ser Ala Lys Leu Glu Arg Leu Tyr Gln Arg Tyr Phe
 130 135 140

Phe Gln Met Asn Gln Ser Ser Leu Thr Leu Leu Met Ala Val Leu Val
 145 150 155 160
 Leu Leu Thr Ala Val Leu Leu Ala Phe His Ala Ala Pro Ala Arg Pro
 165 170 175
 Gln Pro Ala Tyr Val Ala Leu Leu Ala Cys Ala Ala Ala Leu Phe Val
 180 185 190
 Gly Leu Met Val Val Cys Asn Arg His Ser Phe Arg Gln Asp Ser Met
 195 200 205
 Trp Val Val Ser Tyr Val Val Leu Gly Ile Leu Ala Ala Val Gln Val
 210 215 220
 Gly Gly Ala Leu Ala Ala Asp Pro Arg Ser Pro Ser Ala Gly Leu Trp
 225 230 235 240
 Cys Pro Val Phe Phe Val Tyr Ile Ala Tyr Thr Leu Leu Pro Ile Arg
 245 250 255
 Met Arg Ala Ala Val Leu Ser Gly Leu Gly Leu Ser Thr Leu His Leu
 260 265 270
 Ile Leu Ala Trp Gln Leu Asn Arg Gly Asp Ala Phe Leu Trp Lys Gln
 275 280 285
 Leu Gly Ala Asn Val Leu Leu Phe Leu Cys Thr Asn Val Ile Gly Ile
 290 295 300
 Cys Thr His Tyr Pro Ala Glu Val Ser Gln Arg Gln Ala Phe Gln Glu
 305 310 315 320
 Thr Arg Gly Tyr Ile Gln Ala Arg Leu His Leu Gln His Glu Asn Arg
 325 330 335
 Gln Gln Glu Arg Leu Leu Leu Ser Val Leu Pro Gln His Val Ala Met
 340 345 350
 Glu Met Lys Glu Asp Ile Asn Thr Lys Lys Glu Asp Met Met Phe His
 355 360 365
 Lys Ile Tyr Ile Gln Lys His Asp Asn Val Ser Ile Leu Phe Ala Asp
 370 375 380
 Ile Glu Gly Phe Thr Ser Leu Ala Ser Gln Cys Thr Ala Gln Glu Leu
 385 390 395 400
 Val Met Thr Leu Asn Glu Leu Phe Ala Arg Phe Asp Lys Leu Ala Ala
 405 410 415
 Glu Asn His Cys Leu Arg Ile Lys Ile Leu Gly Asp Cys Tyr Tyr Cys
 420 425 430
 Val Ser Gly Leu Pro Glu Ala Arg Ala Asp His Ala His Cys Cys Val
 435 440 445
 Glu Met Gly Val Asp Met Ile Glu Ala Ile Ser Leu Val Arg Glu Val
 450 455 460
 Thr Gly Val Asn Val Asn Met Arg Val Gly Ile His Ser Gly Arg Val
 465 470 475 480
 His Cys Gly Val Leu Gly Leu Arg Lys Trp Gln Phe Asp Val Trp Ser
 485 490 495
 Asn Asp Val Thr Leu Ala Asn His Met Glu Ala Gly Gly Gly Arg Arg

500 505 510
 Ile His Ile Thr Arg Ala Thr Leu Gln Tyr Leu Asn Gly Asp Tyr Glu
 515 520 525
 Val Glu Pro Gly Arg Gly Gly Glu Arg Asn Ala Tyr Leu Lys Glu Gln
 530 535 540
 Cys Ile Glu Thr Phe Leu Ile Leu Gly Ala Ser Gln Lys Arg Lys Glu
 545 550 555 560
 Glu Lys Ala Met Leu Ala Lys Leu Gln Arg Thr Arg Ala Asn Ser Met
 565 570 575
 Glu Gly Leu Met Pro Arg Trp Val Pro Asp Arg Ala Phe Ser Arg Thr
 580 585 590
 Lys Asp Ser Lys Ala Phe Arg Gln Met Gly Ile Asp Asp Ser Ser Lys
 595 600 605
 Asp Asn Arg Gly Ala Gln Asp Ala Leu Asn Pro Glu Asp Glu Val Asp
 610 615 620
 Glu Phe Leu Gly Arg Ala Ile Asp Ala Arg Ser Ile Asp Gln Leu Arg
 625 630 635 640
 Lys Asp His Val Arg Arg Phe Leu Leu Thr Phe Gln Arg Glu Asp Leu
 645 650 655
 Glu Lys Lys Tyr Ser Arg Lys Val Asp Pro Arg Phe Gly Ala Tyr Val
 660 665 670
 Ala Cys Ala Leu Leu Val Phe Cys Phe Ile Cys Phe Ile Gln Leu Leu
 675 680 685
 Ile Phe Pro His Ser Thr Leu Met Leu Gly Ile Tyr Ala Ser Ile Phe
 690 695 700
 Leu Leu Leu Leu Ile Thr Val Leu Ile Cys Ala Val Tyr Ser Cys Gly
 705 710 715 720
 Ser Leu Phe Pro Lys Ala Leu Gln Arg Leu Ser Arg Ser Ile Val Arg
 725 730 735
 Ser Arg Ala His Ser Thr Ala Val Gly Ile Phe Ser Val Leu Leu Val
 740 745 750
 Phe Thr Ser Ala Ile Ala Asn Met Phe Thr Cys Asn His Thr Pro Ile
 755 760 765
 Arg Ser Cys Ala Ala Arg Met Leu Asn Leu Thr Pro Ala Asp Ile Thr
 770 775 780
 Ala Cys His Leu Gln Gln Leu Asn Tyr Ser Leu Gly Leu Asp Ala Pro
 785 790 795 800
 Leu Cys Glu Gly Thr Met Pro Thr Cys Ser Phe Pro Glu Tyr Phe Ile
 805 810 815
 Gly Asn Met Leu Leu Ser Leu Leu Ala Ser Ser Val Phe Leu His Ile
 820 825 830
 Ser Ser Ile Gly Lys Leu Ala Met Ile Phe Val Leu Gly Leu Ile Tyr
 835 840 845
 Leu Val Leu Leu Leu Leu Gly Pro Pro Ala Thr Ile Phe Asp Asn Tyr
 850 855 860

Asp Leu Leu Leu Gly Val His Gly Leu Ala Ser Ser Asn Glu Thr Phe
 865 870 875 880
 Asp Gly Leu Asp Cys Pro Ala Ala Gly Arg Val Ala Leu Lys Tyr Met
 885 890 895
 Thr Pro Val Ile Leu Leu Val Phe Ala Leu Ala Leu Tyr Leu His Ala
 900 905 910
 Gln Gln Val Glu Ser Thr Ala Arg Leu Asp Phe Leu Trp Lys Leu Gln
 915 920 925
 Ala Thr Gly Glu Lys Glu Glu Met Glu Glu Leu Gln Ala Tyr Asn Arg
 930 935 940
 Arg Leu Leu His Asn Ile Leu Pro Lys Asp Val Ala Ala His Phe Leu
 945 950 955 960
 Ala Arg Glu Arg Arg Asn Asp Glu Leu Tyr Tyr Gln Ser Cys Glu Cys
 965 970 975
 Val Ala Val Met Phe Ala Ser Ile Ala Asn Phe Ser Glu Phe Tyr Val
 980 985 990
 Glu Leu Glu Ala Asn Asn Glu Gly Val Glu Cys Leu Arg Leu Leu Asn
 995 1000 1005
 Glu Ile Ile Ala Asp Phe Asp Glu Ile Ile Ser Glu Glu Arg Phe Arg
 1010 1015 1020
 Gln Leu Glu Lys Ile Lys Thr Ile Gly Ser Thr Tyr Met Ala Ala Ser
 1025 1030 1035 1040
 Gly Leu Asn Ala Ser Thr Tyr Asp Gln Val Gly Arg Ser His Ile Thr
 1045 1050 1055
 Ala Leu Ala Asp Tyr Ala Met Arg Leu Met Glu Gln Met Lys His Ile
 1060 1065 1070
 Asn Glu His Ser Phe Asn Asn Phe Gln Met Lys Ile Gly Leu Asn Met
 1075 1080 1085
 Gly Pro Val Val Ala Gly Val Ile Gly Ala Arg Lys Pro Gln Tyr Asp
 1090 1095 1100
 Ile Trp Gly Asn Thr Val Asn Val Ser Ser Arg Met Asp Ser Thr Gly
 1105 1110 1115 1120
 Val Pro Asp Arg Ile Gln Val Thr Thr Asp Leu Tyr Gln Val Leu Ala
 1125 1130 1135
 Ala Lys Gly Tyr Gln Leu Glu Cys Arg Gly Val Val Lys Val Lys Gly
 1140 1145 1150
 Lys Gly Glu Met Thr Thr Tyr Phe Leu Asn Gly Gly Pro Ser Ser
 1155 1160 1165